



# SEQUENCE LISTING

<110> DYAX Corp.  
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Luneau, Christopher J.  
Ladner, Robert C

<120> NOVEL ENTEROKINASE CLEAVAGE SEQUENCES

<130> DYX-012.1 US, DYX-012.1 PCT

<140> 09/884,767  
<141> 2001-06-19

<150> US 09/597,321  
<151> 2000-06-19

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<170> PatentIn version 3.1

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<223> Xaa4 is Ala, Asp, Glu, or Thr

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Xaa Xaa Xaa Xaa Asp Arg Xaa  
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Xaa Xaa Xaa Xaa Glu Arg Xaa  
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Asp Ile Asn Asp Asp Arg Xaa  
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Gly Asn Tyr Thr Asp Arg Xaa  
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Cys His Pro Gln Phe Cys  
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Cys His Pro Gln Phe Cys Ser Trp Arg  
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 c cleavage sites)

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Asp Asp Asp Asp Lys Xaa  
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0984757-091001

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Ala Glu Trp His Pro Gln Phe Ser Ser Pro Ser Ala Ser Arg Pro Ser  
1 5 10 15

Glu Gly Pro Cys His Pro Gln Phe Pro Arg Cys Tyr Ile Glu Asn Leu  
20 25 30

Asp Glu Phe Arg Pro Gly Gly Ser Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Ala Gln Ser Asp Gly Gly Gly Ser  
50 55 60

Thr Glu His Ala Glu Gly Gly Ser Ala Asp Pro Ser Tyr Ile Glu Gly  
65 70 75 80

Arg Ile Val Gly Ser Ala  
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Asn Ser Ile Lys Asp Arg Val  
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09947-04001

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Leu Gly Lys Val Asp Arg Thr  
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Gly His Trp Leu Asp Lys Asn  
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Figure 1 consists of 12 micrographs arranged vertically, labeled 1 through 12. Each micrograph shows a different stage of chick embryo development. 
 1. A single cell (zygote) with a prominent nucleus.
 2. Two cells (2-cell stage).
 3. Four cells (4-cell stage).
 4. Eight cells (8-cell stage).
 5. Morula stage, a solid ball of cells.
 6. Early gastrula stage, showing the beginning of tissue differentiation.
 7. Mid-gastrula stage.
 8. Late gastrula stage.
 9. Early neurulation stage, with the neural tube beginning to form.
 10. Mid-neurulation stage.
 11. Late neurulation stage.
 12. A fully developed chick embryo, ready to hatch from the egg, showing distinct head, body, and tail regions.

**<220>**

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<400> 16

Asn Lys Ala Lys Asp Arg Met

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Ser Glu Asn Phe Asp Lys Asn

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Leu Asp Trp Glu Asp Arg Ala

**1** **5**

**<210> 19**

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Ser Thr Asp Ala Glu Arg Met

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Gly Phe Tyr Asn Asp Arg Met  
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Trp Gln Glu Ser Asp Arg Ala  
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Gly Ser Gly Gly Asp Arg His  
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Gly Ser Gly Gly Glu Arg Thr  
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Pro Asp Pro Gln Glu Arg Gln  
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Tyr Ile Met Gly Asp Arg Thr  
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Gln Asn His Ser Asp Arg Thr  
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Ile Ala His Gly Glu Arg Ala  
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His Glu Met Asn Asp Arg His  
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Thr His Asn Gly Glu Lys Met  
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Gly Tyr Trp Ile Asp Arg Ser  
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Pro Ala His Thr Asp Arg Asp  
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Asp Met Gly Tyr Asp Arg Gly  
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Gly Ser Gly Gly Asp Arg Phe  
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Arg His Asn Tyr Asp Arg Ile  
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Val Tyr His Val Asp Lys Met  
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Gly Gly Lys Tyr Asp Arg Met  
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 Pro Cys Lys Asp Glu Arg Phe  
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 Gly Ser Glu Leu Asp Arg Met  
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Phe Ser Glu Glu Asp Arg Met  
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Gly Ser Gly Gly Glu Arg Phe  
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Tyr Gln Pro Thr Asp Arg Thr  
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Ser Gly Gly Glu Asp Arg Met  
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Thr Glu Gln Met Asp Arg Met  
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Gln Pro Phe Asp Asp Arg Asp  
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Gly Ser Gly Gly Glu Arg Thr  
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Glu Gly Met Thr Asp Arg Leu  
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Figure 1 consists of 12 bar charts arranged in a 6x2 grid. Each chart compares four groups: All respondents, Non-respondents, Respondents who did not receive the survey, and Respondents who received the survey. The variables measured are Age, Sex, Education, Income, Marital status, Religion, Ethnicity, Region, Country, and Attitudes towards the environment and the government. The charts show that the 'Respondents who received the survey' group generally has higher percentages for most variables compared to the other groups.

Variable	All respondents	Non-respondents	Respondents who did not receive the survey	Respondents who received the survey
Age	18-24: 15%, 25-34: 25%, 35-44: 30%, 45-54: 20%, 55-64: 10%	18-24: 10%, 25-34: 20%, 35-44: 30%, 45-54: 25%, 55-64: 15%	18-24: 12%, 25-34: 22%, 35-44: 32%, 45-54: 20%, 55-64: 10%	18-24: 18%, 25-34: 28%, 35-44: 30%, 45-54: 20%, 55-64: 10%
Sex	Male: 55%, Female: 45%	Male: 50%, Female: 50%	Male: 52%, Female: 48%	Male: 58%, Female: 42%
Education	Primary: 10%, Secondary: 30%, Tertiary: 60%	Primary: 15%, Secondary: 40%, Tertiary: 45%	Primary: 12%, Secondary: 35%, Tertiary: 53%	Primary: 8%, Secondary: 25%, Tertiary: 67%
Income	< \$10,000: 10%, \$10,000-\$20,000: 20%, \$20,000-\$30,000: 30%, \$30,000-\$40,000: 20%, > \$40,000: 20%	< \$10,000: 15%, \$10,000-\$20,000: 30%, \$20,000-\$30,000: 30%, \$30,000-\$40,000: 15%, > \$40,000: 10%	< \$10,000: 12%, \$10,000-\$20,000: 25%, \$20,000-\$30,000: 35%, \$30,000-\$40,000: 20%, > \$40,000: 8%	< \$10,000: 18%, \$10,000-\$20,000: 28%, \$20,000-\$30,000: 30%, \$30,000-\$40,000: 20%, > \$40,000: 4%
Marital status	Single: 30%, Married: 40%, Divorced: 10%, Widowed: 20%	Single: 25%, Married: 45%, Divorced: 15%, Widowed: 15%	Single: 28%, Married: 42%, Divorced: 12%, Widowed: 18%	Single: 35%, Married: 40%, Divorced: 10%, Widowed: 15%
Religion	Christian: 60%, Muslim: 30%, Hindu: 5%, Buddhist: 2%, Other: 3%	Christian: 55%, Muslim: 35%, Hindu: 5%, Buddhist: 2%, Other: 3%	Christian: 58%, Muslim: 32%, Hindu: 5%, Buddhist: 2%, Other: 3%	Christian: 65%, Muslim: 28%, Hindu: 5%, Buddhist: 2%, Other: 3%
Ethnicity	White: 60%, Black: 20%, Asian: 10%, Hispanic: 5%, Other: 5%	White: 55%, Black: 25%, Asian: 10%, Hispanic: 5%, Other: 5%	White: 58%, Black: 22%, Asian: 10%, Hispanic: 5%, Other: 5%	White: 65%, Black: 18%, Asian: 10%, Hispanic: 5%, Other: 5%
Region	North: 30%, South: 30%, East: 20%, West: 20%	North: 25%, South: 35%, East: 20%, West: 20%	North: 28%, South: 32%, East: 20%, West: 20%	North: 35%, South: 30%, East: 20%, West: 15%
Country	USA: 60%, Canada: 20%, UK: 10%, Australia: 5%, Other: 5%	USA: 55%, Canada: 25%, UK: 10%, Australia: 5%, Other: 5%	USA: 58%, Canada: 22%, UK: 10%, Australia: 5%, Other: 5%	USA: 65%, Canada: 18%, UK: 10%, Australia: 5%, Other: 5%
Attitudes towards the environment	Strongly agree: 40%, Agree: 30%, Disagree: 10%, Strongly disagree: 20%	Strongly agree: 35%, Agree: 35%, Disagree: 15%, Strongly disagree: 15%	Strongly agree: 38%, Agree: 32%, Disagree: 12%, Strongly disagree: 18%	Strongly agree: 45%, Agree: 30%, Disagree: 10%, Strongly disagree: 15%
Attitudes towards the government	Strongly agree: 30%, Agree: 40%, Disagree: 10%, Strongly disagree: 20%	Strongly agree: 25%, Agree: 45%, Disagree: 15%, Strongly disagree: 15%	Strongly agree: 28%, Agree: 42%, Disagree: 12%, Strongly disagree: 18%	Strongly agree: 35%, Agree: 40%, Disagree: 10%, Strongly disagree: 15%

&lt;223&gt; synthetic enterokinase cleavage sequence

Glu Ile Pro Glu Asp Arg Met

**1** **5**

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<213> Artificial Sequence

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Gly Asp Asp Asp Asp Lys Ile

1 5

<211> 7

<212> PRT

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Gly Ser Gly Gly Glu Arg Ser

1 5

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His Gly Tyr Glu Glu Arg Met

1 5

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Lys Pro Met Glu Glu Arg Met  
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Gly Ser Gly Gly Asp Arg Asn  
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Asp Val Thr Ala Asp Asp Arg  
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<222> (1)..(1)  
 <223> Xaa1 is an optional amino acid which, if present, is Ala, Asp, Glu, Phe, Gly, Ile, Asn, Ser, or Val

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> Xaa2 is an optional amino acid which, if present, is Ala, Asp, Glu, His, Ile, Leu, Met, Gln, or Ser

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(3)  
 <223> Xaa3 is an optional amino acid which, if present, is Asp, Glu, Phe, His, Ile, Met, Asn, Pro, Val, or Trp

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> Xaa4 is Ala, Asp, Glu, or Thr

<220>  
 <221> MISC\_FEATURE  
 <222> (7)..(7)  
 <223> Xaa7 is any amino acid

<400> 206

Xaa Xaa Xaa Xaa Asp Arg Xaa  
 1 5

<210> 207  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic enterokinase cleavage sequence

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(1)  
 <223> Xaa1 is an optional amino acid which, if present, is Asp or Glu

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> Xaa2 is an optional amino acid which, if present, is Val

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(3)  
 <223> Xaa3 is an optional amino acid which, if present, is Tyr

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> Xaa4 is Asp, Glu or Ser

<220>  
 <221> MISC\_FEATURE  
 <222> (7)..(7)  
 <223> Xaa7 is any amino acid

<400> 207  
 Xaa Xaa Xaa Xaa Glu Arg Xaa  
 1 5

<210> 208  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic enterokinase cleavage sequence

<400> 208  
 Asp Ile Asn Asp Asp Arg  
 1 5

<210> 209  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic enterokinase cleavage sequence

<400> 209  
 Gly Asn Tyr Thr Asp Arg  
 1 5

<210> 210  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

098457 094001

<220>  
<223> streptavidin binding sequence

<400> 210

Trp His Pro Gln Phe Ser Ser  
1 5

<210> 211  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> steptavidin binding sequence

<400> 211

Pro Cys His Pro Gln Phe Pro Arg Cys Tyr  
1 5 10

<210> 212  
<211> 1272  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Bacteriophage M13mp18

<400> 212  
gtgaaaaaat tattattcgc aattccttta gttgttcctt tctattctca ctccgctgaa 60  
actggtgaaa gttgttttagc aaaaccccat acagaaaatt catttactaa cgtctggaaa 120  
gacgacaaaa cttagatcg ttacgctaac tatgagggtt gtctgtggaa tgctacaggc 180  
gtttagtatt gtactgggtga cgaaactcag tgttacggta catgggttcc tattgggctt 240  
gctatccctg aaaatgaggg tggtggctct gagggtgagg gttctgaggg tggcggttct 300  
gagggtgagg gtactaaacc tcctgagtag ggtgatacac ctattccggg ctatacttat 360  
atcaaccctc tcgacggcac ttatccgcct ggtactgagc aaaacccgcg taatcctaata 420  
ccttctcttg aggagtctca gcctcttaata actttcatgt ttcagaataa taggttccga 480  
aataggcagg gggcattaac tgtttatacg ggcactgtta ctcaaggcac tgaccccggt 540  
aaaacttatt accagtacac tcctgtatca tcaaaagcca tgtatgacgc ttactggaac 600  
ggtaaattca gagactgagc tttccattct ggctttaatg aagatccatt cgtttgtgaa 660  
tatcaaggcc aatcgtctga cctgcctcaa cctcctgtca atgctggcgg cggctctggt 720  
gggtggttctg gtggcggtc tgagggtggt ggctctgagg gtggcggttc tgagggtggc 780



ggctctgagg gaggcgggttc cggtggtggc tctggttccg gtgattttga ttatgaaaag 840  
atggcaaacg ctaataaggg ggctatgacc gaaaatgccg atgaaaacgc gctacagtct 900  
gacgctaaag gcaaacttga ttctgtcgct actgattacg gtgctgctat cgatgggtttc 960  
attggtgacg tttccggcct tgctaattggt aatggtgcta ctggtgattt tgctggctct 1020  
aattcccaaa tggctcaagt cggtgacggt gataattcac ctttaatgaa taatttccgt 1080  
caatattttac cttccctccc tcaatcggtt gaatgtcgcc cttttgtctt tagcgctggt 1140  
aaaccatatg aattttctat tgattgtgac aaaataaact tattccgtgg tgtctttgcg 1200  
tttcttttat atgttgccac ctttatgtat gtattttcta cgtttgctaa catactgcgt 1260  
aataaggagt ct 1272

<210> 213  
<211> 424  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Bacteriophage M13mp18

<400> 213

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser  
1 5 10 15

His Ser Ala Glu Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu  
20 25 30

Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr  
35 40 45

Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys  
50 55 60

Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu  
65 70 75 80

Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu  
85 90 95

Gly Gly Gly Ser Glu Gly Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp  
100 105 110

0944367 094004

Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr  
115 120 125

Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu  
130 135 140

Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg  
145 150 155 160

Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly  
165 170 175

Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys  
180 185 190

Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe  
195 200 205

His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln  
210 215 220

Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly  
225 230 235 240

Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly  
245 250 255

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly  
260 265 270

Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala  
275 280 285

Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly  
290 295 300

Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe  
305 310 315 320

Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp  
325 330 335

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn  
340 345 350

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln  
355 360 365

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu  
370 375 380

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala  
385 390 395 400

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala  
405 410 415

Asn Ile Leu Arg Asn Lys Glu Ser  
420

<210> 214  
<211> 957  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Bacteriophage M13mp18

<400> 214  
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ggcacttata cgcctggtac tgagcaaaac cccgctaata ctaatccttc tcttgaggag 120  
tctcagcctc ttaatacttt catgtttcag aataataggt tccgaaatag gcagggggca 180  
ttaactgttt atacgggcac tgttactcaa ggcactgacc ccgttaaaac ttattaccag 240  
tacactcctg tatcatcaaa agccatgtat gacgcttact ggaacggtaa attcagagac 300  
tgcgctttcc attctggctt taatgaagat ccattcgttt gtgaatatca aggccaatcg 360  
tctgacctgc ctcaacctcc tgtcaatgct ggcggcggct ctggtggtgg ttctggtggc 420  
ggctctgagg gtggtggctc tgagggtggc ggttctgagg gtggcggctc tgaggggaggc 480  
ggttccgggtg gtggctctgg ttccggtgat tttgattatg aaaagatggc aaacgctaata 540  
aagggggcta tgaccgaaaa tgccgatgaa aacgcgctac agtctgacgc taaaggcaaa 600  
cttgattctg tcgctactga ttacggtgct gctatcgatg gtttcattgg tgacgtttcc 660  
ggccttgcta atggtaatgg tgctactggt gattttgctg gctctaattc ccaaattggct 720

caagtcggtg acggtgataa ttcaccttta atgaataatt tccgtcaata tttaccttcc 780  
ctccctcaat cgggtgaatg tcgccctttt gtcttttagcg ctggtaaacc atatgaattt 840  
tctattgatt gtgacaaaat aaacttattc cgtgggtgtct ttgcgtttct tttatatggt 900  
gccaccttta tgtatgtatt ttctacgttt gctaacatac tgcgtaataa ggagtct 957

<210> 215  
<211> 319  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> Bacteriophage M13mp18  
  
<400> 215

Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr Ile  
1 5 10 15  
  
Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala  
20 25 30  
  
Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met  
35 40 45  
  
Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr  
50 55 60  
  
Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln  
65 70 75 80  
  
Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly  
85 90 95  
  
Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe  
100 105 110  
  
Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val  
115 120 125  
  
Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly  
130 135 140  
  
Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly  
145 150 155 160

Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met  
165 170 175

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala  
180 185 190

Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr  
195 200 205

Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn  
210 215 220

Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala  
225 230 235 240

Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln  
245 250 255

Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe  
260 265 270

Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn  
275 280 285

Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met  
290 295 300

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser  
305 310 315

<210> 216  
<211> 450  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Bacteriophage M13mp18

<400> 216  
gatttttgatt atgaaaagat ggcaaacgct aataaggggg ctatgaccga aaatgccgat 60  
gaaaacgcgc tacagtctga cgctaaaggc aaacttgatt ctgtcgctac tgattacggt 120  
gctgctatcg atggtttcat tggtgacgtt tccggccttg ctaatggtaa tgggtgctact 180

ggtgattttg ctggctctaa ttcccaaagt gctcaagtcg gtgacggtga taattcacct 240  
 ttaatgaata atttccgtca atatttacct tccctccctc aatcggttga atgtcgccct 300  
 tttgtcttta gcgctggtaa accatatgaa ttttctattg attgtgacaa aataaactta 360  
 ttccgtgggtg tctttgcgtt tcttttatat gttgccacct ttatgtatgt attttctacg 420  
 tttgctaaca tactgcgtaa taaggagtct 450

<210> 217  
 <211> 150  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Bacteriophage M13mp18

<400> 217

Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr  
 1 5 10 15

Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu  
 20 25 30

Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly  
 35 40 45

Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala  
 50 55 60

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro  
 65 70 75 80

Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val  
 85 90 95

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser  
 100 105 110

Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu  
 115 120 125

Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile  
 130 135 140

Leu Arg Asn Lys Glu Ser  
145 150

05834757 091001  
TOT60 29243860